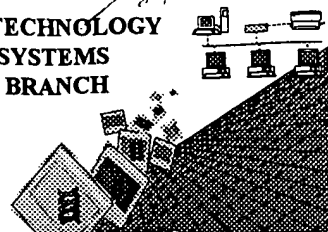


CS/C  
2/26  
BIOTECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/855,587  
Source: OLPE  
Date Processed by STIC: 2/13/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/855,587

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

Global  
error



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/855,587

DATE: 02/13/2002

TIME: 09:39:23

Input Set : A:\766.44 Sequence Listing.txt

Output Set: N:\CRF3\02132002\I855587.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Yoshiki SASAI  
4 Shin-Ichi NISHIKAWA  
6 <120> TITLE OF INVENTION: NOVEL DIFFERENTIATION INDUCING PROCESS OF EMBRYONIC STEM  
CELL  
7 TO ECTODERMAL CELL AND ITS USE  
9 <130> FILE REFERENCE: 766.44  
11 <140> CURRENT APPLICATION NUMBER: US/09/855,587  
11 <141> CURRENT FILING DATE: 2002-01-29  
11 <150> PRIOR APPLICATION NUMBER: JP 2000-144059  
W--> 12 <151> PRIOR FILING DATE: 2000/05/16 2000-05-16  
14 <150> PRIOR APPLICATION NUMBER: JP 2000-290819  
W--> 15 <151> PRIOR FILING DATE: 2000/09/25 2000-09-25  
17 <160> NUMBER OF SEQ ID NOS: 6

use this date format

## ERRORED SEQUENCES

65 <210> SEQ ID NO: 6  
66 <211> LENGTH: 13  
67 <212> TYPE: DNA  
68 <213> ORGANISM: Artificial Sequence  
W--> 69 <220> FEATURE:  
69 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA  
71 <400> SEQUENCE: 6  
72  
E--> 95  
2/2ny\_maIn 231036v1  
tccaccaccc tgggtgctgta g 21  
2217, 2227, or 2237  
is shown  
see item 1 on EMBL summary sheet

The types of errors shown exist throughout the Sequence Listing. Please check all sequences for similar errors.

DO NOT use TAB codes  
in the Sequence Listing file.  
They cause format errors.

Please consult  
Sequence Rules for  
valid format.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/855,587

DATE: 02/13/2002

TIME: 09:39:24

Input Set : A:\766.44 Sequence Listing.txt

Output Set: N:\CRF3\02132002\I855587.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:12 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:23 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:32 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:41 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:51 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:60 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:69 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:95 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6  
L:95 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6  
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:95 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:30 SEQ:6  
L:95 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11  
L:95 M:112 C: (48) String data converted to lower case,  
L:95 M:252 E: No. of Seq. differs, <211>LENGTH:Input:13 Found:30 SEQ:6